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SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: Spurlock, Michael E.
- (ii) TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID SEQUENCES CODING THEREFOR AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: WHYTE HIRSCHBOECK DUDEK S.C.
 - (B) STREET: Suite 2100 111 East Wisconsin Avenue
 - (C) CITY: Milwaukee
 - (D) STATE: Wisconsin
 - (E) COUNTRY: USA
 - (F) ZIP: 53202
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/688,908
 - (B) FILING DATE: 31-JUL-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Plotecher, Gary R.
 - (B) REGISTRATION NUMBER: 27,830
 - (C) REFERENCE/DOCKET NUMBER: PM-8808
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 414-273-2100
 - (B) TELEFAX: 414-223-5000

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATCCGGTC TCAGGCCGTG CCYATCCARA AAGTCC

36

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCAGCG CTGCAYYCAG GGCTRASRTC

30

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 6..443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGGCC GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA ACC CTC ATC	47
Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile	
1 5 10	
AAG ACA ATT GTC ACC AGG ATC AAT GAC ATC TCA CAC ACG CAG TCC GTC	95
Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val	
15 20 25 30	
TCC TCC AAA CAG AGG GTC ACT GGT TTG GAC TTC ATC CCT GGG CTC CAC	143
Ser Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His	
35 40 45	
CCT CTC CTG AGT TTG TCC AAG ATG GAC CAG ACA TTG GCG ATC TAC CAA	191
Pro Leu Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln	
50 55 60	
CAG ATC CTC ACC AGT CTG CCT TCC AGA AAT GTG GTC CAA ATA TCC AAT	239
Gln Ile Leu Thr Ser Leu Pro Ser Arg Asn Val Val Gln Ile Ser Asn	
65 70 75	
GAC CTG GAG AAC CTC CGG GAC CTT CTC CAC CTG CTG GCC GCC TCC AAG	287
Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Ala Ser Lys	
80 85 90	
AGC TGC CCC TTG CCG CAG GTC AGG GCC CTG GAG AGC TTG GAG AGC TTG	335
Ser Cys Pro Leu Pro Gln Val Arg Ala Leu Glu Ser Leu Glu Ser Leu	
95 100 105 110	
GGT GTC GTC CTG GAA GCC TCC CTC TAC TCC ACC GAG GTG GTG GCC CTG	383
Gly Val Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu	
115 120 125	
AGC CGG CTG CAG GGG TCA CTA CAG GAC ATG TTG CGG CAG CTG GAC CTC	431
Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Arg Gln Leu Asp Leu	
130 135 140	

AGC CCT GAA TGC AGCGCT
 Ser Pro Glu Cys
 145

449

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
 1 5 10 15
 Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ser
 20 25 30
 Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Leu
 35 40 45
 Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile
 50 55 60
 Leu Thr Ser Leu Pro Ser Arg Asn Val Val Gln Ile Ser Asn Asp Leu
 65 70 75 80
 Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Ala Ser Lys Ser Cys
 85 90 95
 Pro Leu Pro Gln Val Arg Ala Leu Glu Ser Leu Glu Ser Leu Gly Val
 100 105 110
 Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
 115 120 125
 Leu Gln Gly Ser Leu Gln Asp Met Leu Arg Gln Leu Asp Leu Ser Pro
 130 135 140
 Glu Cys
 145

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 445 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTGTGCC CATCAAAAA GTCCAAGATG ACACCAAAAC CCTCATCAAG ACAATTGTCA 60
 CCAGGATCAA TGACATTTC CACACGCAGT CAGTCTCCTC CAAACAGAAA GTCACCGGTT 120

TGGA	CTTCAT	TCCT	GGGCTC	CACCCC	ATCC	TGAC	CTTATC	CAAG	ATGGAC	CAGAC	ACTGG	180
CAGT	CTACCA	ACAG	ATCCTC	ACCAG	TATGC	CTTC	CAGAAA	CGTG	ATCCAA	ATAT	CCAACG	240
ACCT	GGAGAA	CCTC	CGGGAT	CTTCT	TACG	TGCT	GGCCTT	CTCT	AAGAGC	TGCC	ACTTGC	300
CCTG	GGCCAG	TGGC	CTGGAG	ACCT	TGGACA	GCCT	GGGGGG	TGT	CCTGGAA	GCTT	CAGGCT	360
ACTC	CACAGA	GGTG	GTGGCC	CTGAG	CAGGC	TGCAG	GGGTC	TCTG	CAGGAC	ATGCT	GTGGC	420
AGCT	GGACCT	CAGC	CTGGG	TGCTG								445

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 445 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGTGCC	TATCCAGAAA	GTCCAGGATG	ACACCAAAAC	CCTCATCAAG	ACCATTGTCA	60
CCAGGATCAA	TGACATTTCA	CACACGCAGT	CGGTATCCGC	CAAGCAGAGG	GTC	ACTGGCT 120
TGGA	CTTCAT	TCCT	GGGCTT	CACCCC	ATTC	TGAGTTTGTG 180
CAAG	ATGGAC	CAGACT	CTGG			
CAGT	CTATCA	ACAGGT	CCTC	ACCAG	CCTGC	CTTCCCAAAA 240
TGTG	CTGCAG	ATAG	CCAATG			
ACCT	GGAGAA	TCTCC	GAGAC	CTCCT	CCATC	TGCTGGCCTT 300
CTCCA	AAGAGC	TGCT	CCCTGC			
CTCAG	ACCAG	TGGC	CTGCAG	AAGCC	CAGAGA	GCCTGGATGG 360
CGTC	CCTGGAA	GCCT	CACTCT			
ACTC	CACAGA	GGTG	GTGGCT	TTGAG	CAGGC	TGCAGGGCTC 420
TCTG	CAGGAC	ATTCT	TCAAC			
AGTT	GGATGT	TAGCC	CTGAA	TGCTG		445

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	His	Trp	Gly	Thr	Leu	Cys	Gly	Phe	Leu	Trp	Leu	Trp	Pro	Tyr	Leu
1				5					10					15	
Phe	Tyr	Val	Gln	Ala	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys
			20					25					30		

Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
 35 40 45
 Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
 50 55 60
 Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
 65 70 75 80
 Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
 85 90 95
 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
 100 105 110
 Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
 115 120 125
 Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
 130 135 140
 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
 145 150 155 160
 Leu Asp Leu Ser Pro Gly Cys
 165

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
 1 5 10 15
 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
 20 25 30
 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
 35 40 45
 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
 50 55 60
 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
 65 70 75 80
 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
 85 90 95
 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
 100 105 110
 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
 115 120 125

Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
130 135 140

Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
145 150 155 160

Leu Asp Val Ser Pro Glu Cys
165